DRAWINGS

FIG. 1

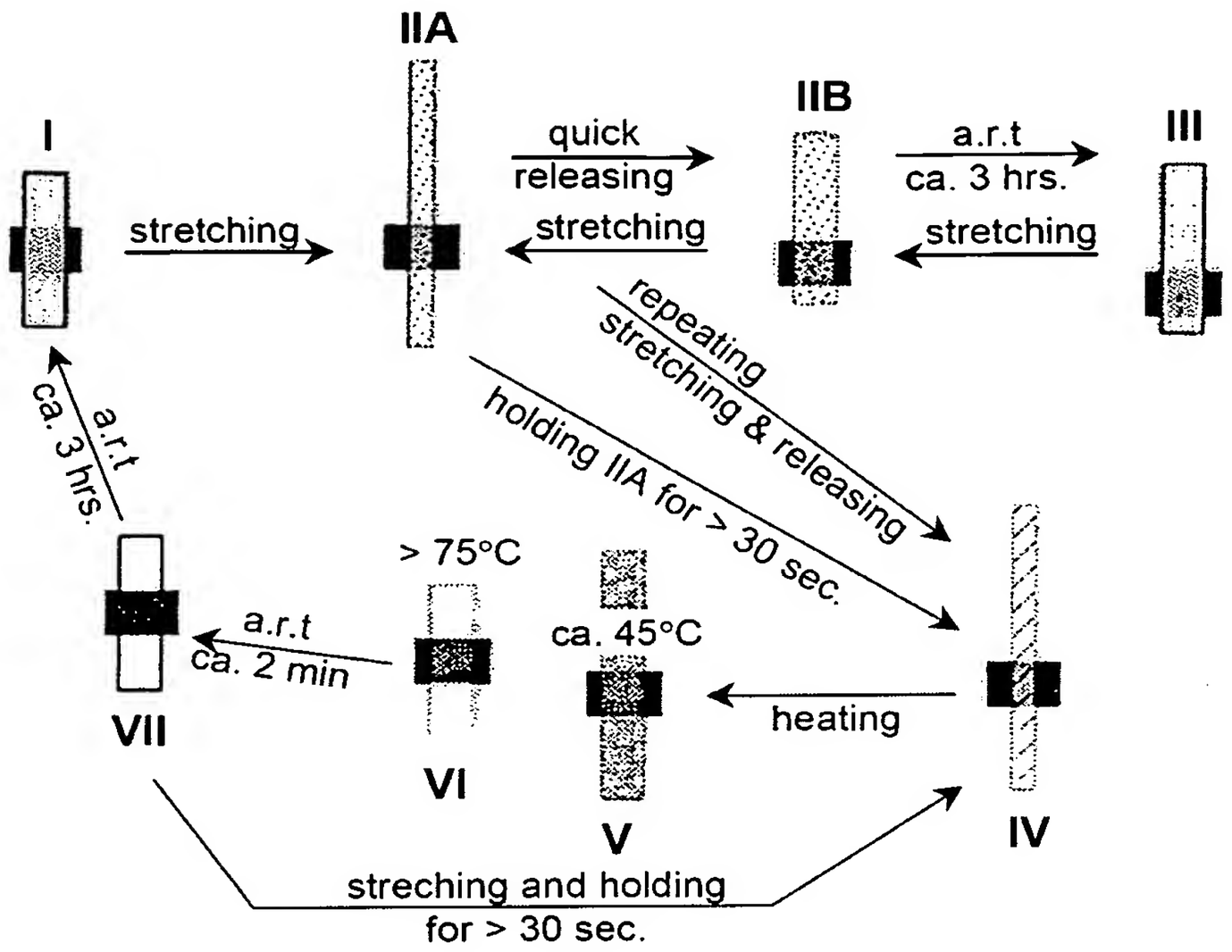


FIG. 2

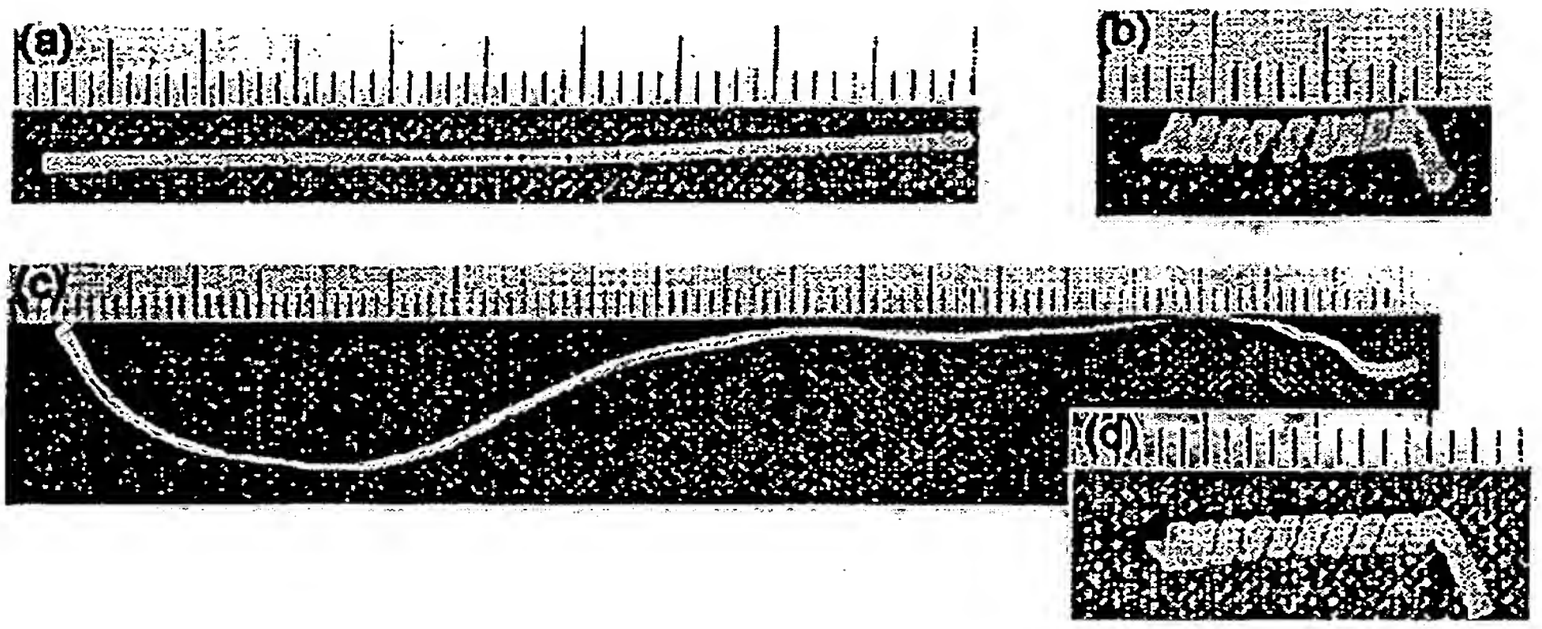


FIG. 3

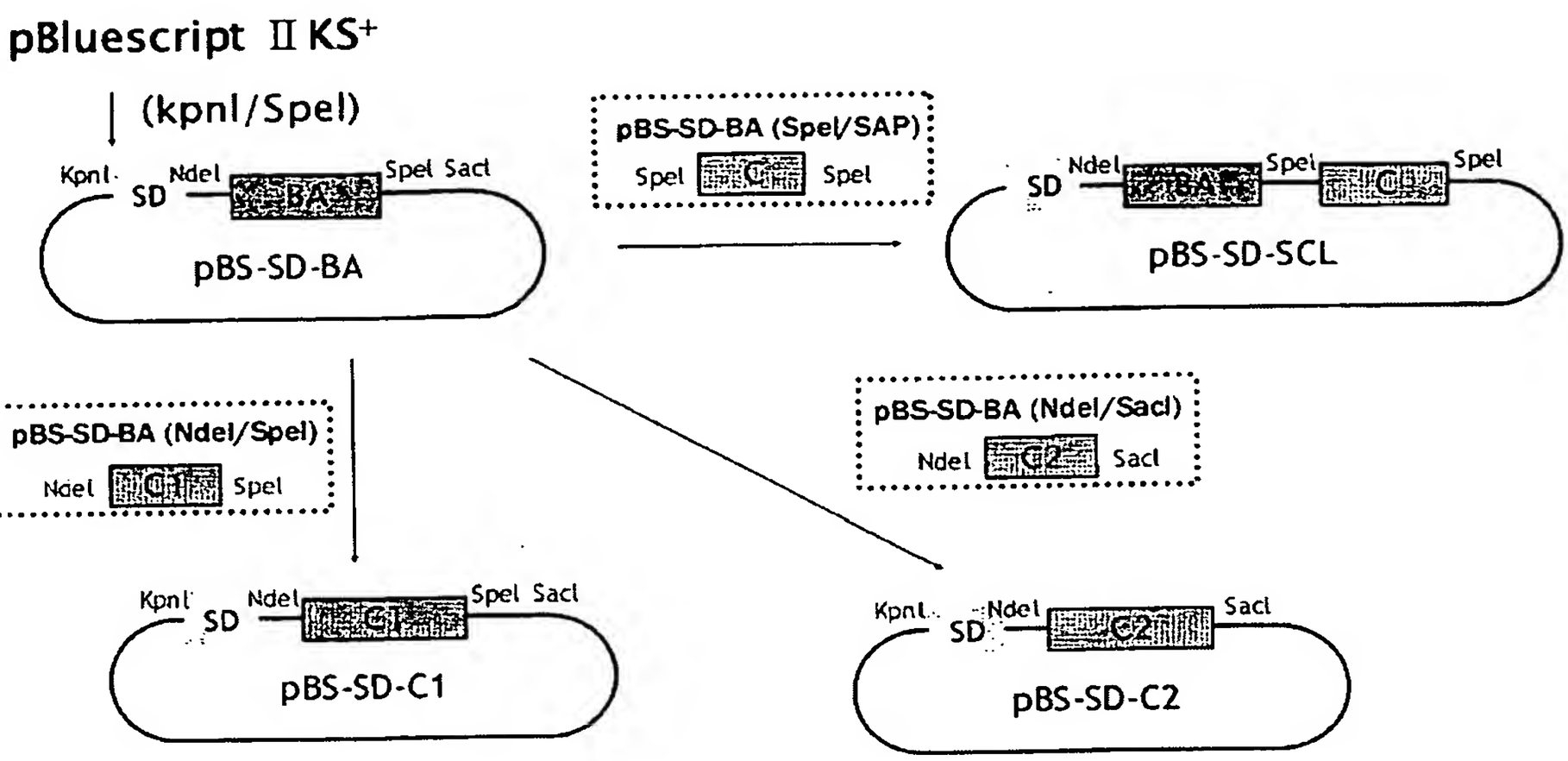
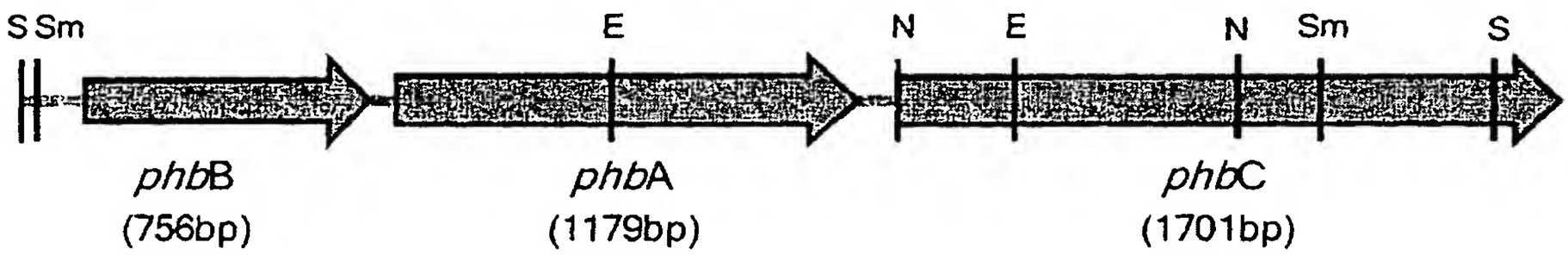


FIG. 4



SCL-PHA locus

3933bp

phbC locus

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1     GAGCTCAATG CGCGCCAGGA CTGGTGTGCG AGGACAACCC GGCGTCACCC GGGGACATTG TTCACATCCG CAAAGCGCCA GAGACTTGCC CGCTGTTCCA AGGTCTTAAT TAACGAGGAA
      phbB ──►
          M  G  T  A  S  N  A  A  R  I  A  L  V  T  G  G  M  G  G  I  G  T  A  I  S  Q  R  L  H  R  D  G  F  T  V  V  V  G
121   TGGTTAATGG GTACTGCGAG CAATGCGGCA CGTATAGCTC TGGTCACCGG TGGTATGGGC GGTATCGGTA CGGCGATCAG CCAGCGCCTG CATCGGGATG GCTTCACCGT GGTGGTGGGC
      C  N  P  Y  S  S  R  K  A  S  W  I  A  T  Q  L  E  A  G  F  H  F  H  C  I  D  C  D  I  T  D  W  D  S  T  R  Q  A  F  D
241   TGTAATCCCT ACTCCAGCCG CAAGGCTTCC TGGATTGCCA CGCAACTCGA GGCGGGCTTT CACTTCCACT GCATCGACTG CGACATCACC GACTGGGATA GCACCCGCCA GGCCTTCGAC
      M  V  H  E  T  V  G  P  I  D  V  L  V  N  N  A  G  I  T  R  D  G  T  F  R  K  M  S  P  E  N  W  K  A  V  I  D  T  N  L
361   ATGGTGCACG AGACTGTCGG CCCGATCGAT GTATTGGTCA ACAATGCCGG CATCACCCGC GACGGCACTT TCCGCAAGAT GTCCCCGGAA AACTGGAAGG CGGTGATCGA TACCAATCTC
      T  G  L  F  N  T  T  K  Q  V  I  E  G  M  L  A  K  G  W  G  R  V  I  N  I  S  S  I  N  G  Q  R  G  Q  F  G  Q  T  N  Y
481   ACCGGCCTGT TCAACACAAC CAAGCAGGTC ATCGAGGGCA TGCTGGCCAA GGGCTGGGGA CGCGTCATCA ACATCTCCTC AATCAATGGC CAGCGAGGCC AGTTCGGGCA GACCAACTAC
      S  A  X  K  A  G  I  H  G  F  S  M  A  L  A  R  E  V  S  G  K  G  V  T  V  N  T  V  S  P  G  Y  I  K  T  D  M  T  A  A
601   TCCGCGGNCA AGGCTGGCAT TCATGGCTTC AGCATGGCCT TGGCCCGCGA GGTGAGTGGC AAGGGCGTGA CCGTCAATAC GGTTTCCCCT GGCTACATCA AGACCGACAT GACCGCGGCG
      I  R  P  D  I  L  E  D  M  I  T  G  I  P  V  G  R  L  G  Q  P  E  E  I  A  S  I  V  A  W  L  A  S  D  Q  S  A  Y  A  T
721   ATTCGCCCGG ACATCCTCGA AGACATGATT ACTGGCATTC CCGTGGGCCG TCTCGGCCAG CCCGAGGAGA TCGCCTCGAT CGTGGCCTGG CTGGCCTCCG ATCAGTCTGC CTATGCCACC
                                                                                                                  phbA ──►
      G  A  D  F  S  V  N  G  G  M  N  M  Q  *                                                                   M  I  E  V  V  I  V  A  A  T  R
841   GGCGCCGACT TCTCGGTGAA TGGCGGCATG AACATGCAGT GATGCGCCAT TCGCGCCCTC GCTCAGCCAT GACATGAGGT GTTCCAGATG ATCGAAGTCG TTATCGTCGC CGCCACTCGC
      T  A  I  G  A  F  Q  G  S  L  A  G  T  P  A  V  E  L  G  A  T  V  I  R  R  L  L  E  Q  T  A  L  D  S  S  Q  V  D  E  V
961   ACCGCCATCG GCGCTTTCCA GGGGAGCCTG GCCGGCACTC CCGCCGTTGA ACTGGGCGCC ACGGTGATCC GCCGCCTGCT CGAACAGACC GCTCTGGATA GCAGTCAGGT GGATGAAGTG
      I  L  G  H  V  L  T  A  G  A  G  R  I  P  L  A  R  X  X  V  I  A  G  L  P  H  A  V  P  A  M  T  L  N  K  V  C  G  S  G
1081  ATACTCGGCC ACGTACTCAC CGCCGGTGCT GGCAGAATAC CGCTCGCCAG GCANCNGGTC ATCGCCGGCC TGCCACACGC CGTACCGGCG ATGACCCTGA ACAAGGTCTG TGGCTCCGGC
      L  K  A  L  H  L  G  A  Q  A  I  R  C  G  D  A  E  V  V  I  A  G  G  M  E  N  M  S  L  S  S  Y  V  L  P  K  A  R  T  G
1201  CTGAAAGCCC TGCACCTGGG CGCCCAGGCC ATCCGCTGTG GCGATGCCGA GGTGGTGATT GCCGGTGGCA TGGAGAACAT GAGCCTGTCG TCCTATGTCC TGCCCAAGGC CCGCACCGGC
      L  R  M  G  H  A  Q  L  V  D  S  M  I  V  D  G  L  W  D  A  F  N  D  Y  H  M  G  I  T  A  E  N  L  V  D  K  Y  G  I  S
1321  CTGCGCATGG GCCACGCGCA GCTGGTCGAC AGCATGATCG TCGACGGCCT GTGGGACGCC TTCAACGACT ACCACATGGG GATCACTGCC GAGAACCTGG TAGACAAGTA CGGCATCAGC
      R  E  A  Q  D  E  F  A  A  A  S  Q  Q  K  A  V  A  A  I  E  T  G  R  F  R  D  E  I  V  P  V  S  I  P  Q  R  K  G  E  A
1441  CGCGAAGCCC AGGACGAATT CG CGCCGCC TCGCAGCAGA AAGCCGTGGC CGCCATCGAG ACCGGTCGCT TCCGCGACGA GATCGTCCCG GTGAGCATTC CGCAGCGCAA GGGCGAGGCG
      L  S  F  D  T  D  E  Q  P  R  A  G  T  T  A  E  S  L  G  K  L  K  P  A  F  K  N  D  G  S  V  T  A  G  N  A  S  S  L  N
1561  CTGAGCTTCG ACACCGACGA ACAGCCACGC GCCGGCACCA CCGCCGAGTC GCTGGGCAAG CTGAAACCGG CCTTCAAGAA CGACGGCAGC GTTACTGCCG GCAACGCTTC CAGTCTCAAC
      D  G  A  A  A  V  L  L  M  S  A  A  K  A  A  A  L  G  L  P  V  L  A  K  I  A  A  Y  A  N  A  G  V  D  P  A  I  M  G  I
1681  GACGGCGCCG CCGCGGTACT GCTGATGAGT GCGGCAAAGG CCGCAGCGCT TGGTCTGCCA GTGCTGGCGA AGATCGCCGC CTACGCCAAT GCCGGCGTCG ACCCGGCGAT CATGGGTATC
      G  P  V  S  A  T  R  S  C  L  E  K  A  G  W  S  L  A  E  L  D  L  I  E  A  N  E  A  F  A  A  Q  A  L  A  V  G  Q  E  L
1801  GGACCGGTGT CGGCCACCCG CAGTTGCCTG GAGAAGGCGG GCTGGAGTCT GGCAGAGCTG GATCTGATCG AGGCCAATGA AGCCTTCGCG GCCCAGGCCC TGGCCGTGGG TCAGGAGCTG
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FIG. 5

FIG. 6

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      G  W  D  A  G  R  V  N  V  N  G  G  A  I  A  L  G  H  P  I  G  A  S  G  C  R  V  L  V  S  L  L  H  E  M  L  R  R  D  A
1921  GGCTGGGATG CTGGCAGGGT TAACGTCAAC GGCGGCGCCA TCGCCCTCGG CCACCCCATT GGCGCCTCCG GCTGCCGCGT ACTGGTCAGC CTGCTGCATG AAATGCTCAG GCGCGACGCG
      K  K  G  L  A  T  L  C  I  G  G  G  Q  G  V  A  L  A  I  E  R  *
2041  AAAAAAGGCC TCGCTACCCT GTGTATCGGT GGCGGCCAGG GCGTGGCGCT GGCCATCGAG CGCTGAGTGA CGCTTTCGCG ACTCTGCCGG ACGTGCCCCC CTGCACCCGC ACCGCCAGGC
                                                                                    phbC ──▶
                                                                                    M  D  N  G  H  T  F  A  H  Y  W  S  G  Q  A  P
2161  TGGCCGTGCG GTTACGTCTC GACATGATCG CACCGCGGGC GCGGCTTTTG TTTTCATATT CCTGGAGACG CCATGGACAA CGGACACACC TTTGCTCACT ACTGGTCGGG TCAGGCGCCC
      F  I  A  S  F  V  L  Q  Q  L  R  L  Y  V  A  Q  N  T  W  F  S  G  H  D  Q  S  Q  W  F  D  V  P  V  E  A  L  E  Q  L  Q
2281  TTCATCGCCA GCTTCGTCCT GCAGCAACTG CGCTTATACG TGGCGCAAAA TACTTGGTTC AGCGGGCACG ACCAAAGCCA GTGGTTCGAC GTACCTGTCG AGGCGTTGGA GCAACTGCAG
      A  D  Y  Q  Q  Q  W  A  E  L  G  Q  Q  L  L  S  C  Q  P  F  A  F  S  D  R  R  F  A  S  G  N  W  S  E  P  L  F  G  S  L
2401  GCGGACTACC AACAACAGTG GGCCGAACTT GGCCAGCAAT TGCTGAGCTG CCAGCCGTTC GCATTCAGCG ATCGTCGCTT CGCCAGTGGC AACTGGAGCG AACCGCTGTT CGGTTCCCTG
      A  A  F  Y  L  L  N  S  G  F  L  L  K  L  L  E  L  L  P  I  D  E  Q  K  P  R  Q  R  L  R  Y  L  I  E  Q  A  I  A  A  S
2521  GCTGCCTTCT ACCTGCTGAA TTCCGGTTTC CTGCTGAAAC TGTTGGAGCT TCTCCCCATC GATGAGCAGA AGCCCCGCCA GCGCTTGCGT TACTTGATCG AGCAAGCGAT TGCCGCAAGC
      A  P  S  N  F  L  L  S  N  P  D  A  L  Q  R  L  V  E  T  Q  G  A  S  L  L  S  G  L  L  H  L  A  S  D  L  Q  A  G  K  L
2641  GCCCCAAGTA ACTTTCTGCT GAGCAACCCT GATGCCCTGC AACGCCTAGT GGAAACCCAG GGCGCCAGCC TACTAAGTGG CCTGTTGCAT CTTGCCAGTG ACCTGCAGGC AGGCAAGTTG
      R  Q  C  D  L  G  D  F  E  V  G  V  N  L  A  T  T  P  G  A  V  V  L  E  T  P  L  F  Q  L  I  Q  Y  S  P  L  S  E  T  Q
2761  CGCCAATGTG ACTTGGGCGA TTTCGAAGTC GGCGTGAATC TGGCCACCAC CCCTGGTGCC GTGGTACTGG AAACCCCTCT GTTCCAGCTG ATCCAGTATT CGCCGCTCAG CGAAACGCAA
      Y  Q  R  P  I  F  M  V  P  P  W  I  N  K  Y  Y  I  L  D  L  G  P  E  N  S  L  I  R  H  L  L  E  R  G  H  Q  V  F  L  M
2881  TACCAGCGGC CGATATTCAT GGTCCCGCCC TGGATCAACA AGTACTACAT CCTTGACCTC GGGCCCGAAA ACTCTCTAAT CCGTCATCTA CTGGAGCGAG GCCATCAAGT TTTTCTGATG
      S  W  R  N  F  T  Q  E  Q  A  D  I  T  W  E  Q  I  I  Q  D  G  V  I  S  A  L  R  T  T  R  A  I  S  G  E  R  H  L  N  C
3001  TCCTGGCGCA ACTTCACTCA GGAACAGGCC GACATCACCT GGGAGCAGAT CATCCAGGAC GGAGTGATCA GCGCCCTGCG CACTACCCGG GCCATCAGTG GTGAGCGCCA CCTGAACTGT
      L  G  F  C  I  G  G  T  M  L  S  C  A  L  A  V  L  A  A  R  G  D  Q  D  I  A  S  L  S  L  F  A  T  F  L  D  Y  L  D  T
3121  TTGGGTTTCT GCATCGGCGG CACCATGCTG AGTTGCGCTC TAGCGGTGCT GGCAGCGCGT GGCGACCAGG ACATTGCCAG CCTGAGTCTA TTCGCCACTT TTCTTGACTA CCTTGATACC
      G  P  I  S  V  F  V  D  E  Q  L  V  A  Y  R  E  R  T  I  G  G  H  G  G  K  C  G  L  F  R  G  E  D  M  G  N  T  F  S  L
3241  GGGCCGATCA GCGTCTTCGT CGATGAGCAA CTGGTGGCCT ACCGTGAGCG CACCATCGGT GGCCATGGTG GCAAATGTGG CCTGTTCCGC GGTGAGGACA TGGGCAATAC CTTCTCCCTG
      L  R  P  N  E  L  W  W  N  Y  N  V  D  K  Y  L  K  G  Q  K  P  L  A  L  G  L  L  F  W  N  N  D  S  T  N  L  P  G  P  L
3361  CTGCGGCCCA ACGAGCTGTG GTGGAACTAC AACGTAGACA AATATCTCAA GGGGCAGAAG CCGCTGGCTC TGGGTCTACT GTTCTGGAAC AACGACAGCA CCAATCTGCC GGGGCCCCTG
      Y  C  W  Y  L  R  H  T  Y  L  Q  N  D  L  K  S  G  E  L  D  L  C  G  V  K  L  D  L  R  A  I  D  A  P  A  Y  I  L  G  T
3481  TATTGCTGGT ATCTGCGCCA CACCTACCTG CAGAACGACC TCAAATCGGG GGAGTTGGAT CTGTGCGGCG TCAAGTTGGA TCTGCGGGCC ATAGACGCAC CAGCCTACAT CTTGGGAACC
      H  D  D  H  I  V  P  W  R  S  A  Y  A  S  T  E  L  L  G  G  P  K  R  F  V  L  G  A  S  G  H  I  A  G  V  I  N  P  P  D
3601  CATGACGACC ACATCGTGCC CTGGCGAAGC GCCTATGCCA GCACGGAATT GCTGGGAGGT CCAAAGCGCT TTGTCCTCGG CGCCTCCGGC CACATCGCCG GGGTGATCAA CCCGCCAGAT
      R  N  K  R  H  Y  W  V  N  E  H  I  A  P  V  A  D  D  W  L  Q  G  A  Q  Q  H  S  G  S  W  W  G  D  W  F  A  W  L  T  G
3721  AGGAACAAGC GCCATTACTG GGTCAATGAA CACATAGCGC CGGTAGCTGA CGACTGGCTG CAGGGAGCTC AGCAGCATTC CGGCAGTTGG TGGGGTGACT GGTTCGCCTG GTTGACCGGC
      Y  A  G  P  R  K  P  A  I  T  M  L  G  S  A  E  Y  P  P  L  E  H  A  P  G  R  Y  V  K  L  *
3841  TATGCCGGCC CACGCAAGCC TGCCATCACT ATGCTGGGCA GTGCCGAGTA CCCCCCGCTT GAACATGCGC CAGGACGTTA TGTGAAGCTA TGA
```